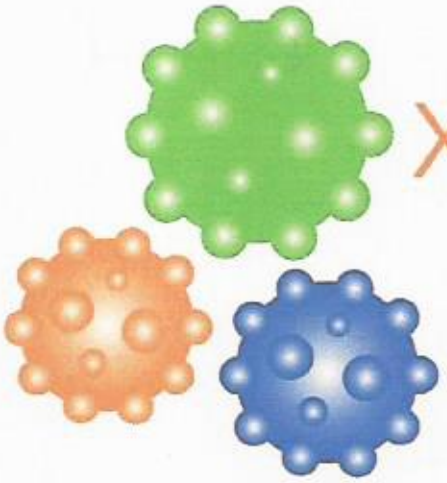
Bat Coronaviruses circulating in Danish bats

Rasmussen, Thomas Bruun; Chriél, Mariann; Baagøe, Hans J.; Fjederholt, Esben; Kooi, Engbert A.; Belsham, Graham; Bøtner, Anette

Published in:
Xth International Congress for Veterinary Virology

Publication date:
2015

Document Version
Publisher's PDF, also known as Version of record



Xth International Congress for Veterinary Virology

9th Annual Meeting of EPIZONE

Changing Viruses in a Changing World

August 31st - September 3rd 2015

Le Corum, Montpellier, France

Topic: Domestic & wild life virus interaction

Bat Coronaviruses circulating in Danish bats

Thomas Bruun Rasmussen [1], Mariann Chriél [1], Hans Baagøe [2], Esben Fjederholt [2], Engbert Kooi [3], Graham J. Belsham [1], Anette Bøtner [1]

1: DTU National Veterinary Institute (DTUVet) - DK-4771 Kalvehave - Denmark
2: The Natural History Museum of Copenhagen (Copenhagen University) - Denmark
3: Central Veterinary Institute (CVI) - Netherlands

Objective: Coronaviruses (CoVs) are a diverse group of large positive-stranded RNA viruses. Several CoVs are known to cause severe diseases in animals (e.g. PED and TGE) and humans (e.g. SARS and MERS). Bat populations worldwide are considered to be natural reservoirs for many diverse CoVs. However, incomplete information exists about the bat species hosting specific CoVs and also the nature of bat CoVs circulating in Europe. In this study, we investigated Danish healthy bat populations for the presence of CoVs.

Methods: Fecal samples were collected during the autumn of 2013 and 2014 from 10 out of 17 Danish species of bats caught alive and released after sampling. The samples were screened for the presence of CoV RNA using pan-CoV RT-qPCRs targeting conserved regions of the ORF1ab that encodes the viral RNA polymerase. Amplicons that were generated were sequenced to confirm the presence of CoV and to determine the type and diversity of CoVs among Danish bat species.

Results: CoV RNAs were detected in 4 of the 10 Danish bat species: M. daubentonii, M. nattereri, P. pygmaeus and E. serotinus. The nucleotide sequencing revealed distinct CoV sequences within each of the four bat species indicating that specific CoVs are confined to single host species.

Conclusion: Our results show, for the first time, that several different bat CoVs are present in the Danish bat population.

Prevalence of Avian Corona Viruses in samples collected for passive avian influenza surveillance on wildbirds in Sweden

Siamak Zohari [1], Annie Persson [1], Linda Forslund [1], Henrik Uhlhorn [2], Caroline Bröjer [2], Jean-François Valarcher [3], Lena Renstrom [1]

1: Department of Virology, Immunobiology and Parasitology (SVA) - Statens Veterinärmedicinska Anstalt, SVA SE-75189 Uppsala - Sweden
2: Department of Pathology and Wildlife Diseases, Wildlife Section (SVA), Statens veterinärmedicinska Anstalt, SVA SE-75189 Uppsala - Sweden
3: Swedish University of Agricultural Sciences, Department of Clinical Science (SLU), Ulls väg 26, 75007 Uppsala - Sweden

Objective: The knowledge of the prevalence of AvCoVs in wild bird's species is limited. With exception of isolates from chickens, turkey, guinea fowl and peasant, only a small number of experimental studies have been carried out to study host range of avian CoVs in Europe. Here we will discuss the prevalence of AvCoVs in 407 samples collected from 87 different bird species in 2013.

Methods: The survey in wild birds in Sweden is consists of both active surveillance on living birds and passive surveillance on birds found dead or diseased. The active surveillance was primarily targeting high risk species for avian influenza in accordance with Commission decision 2007/268/ EC, Annex II. However within the passive surveillance birds from different species where sampled which was carried out by national veterinary institute. From dead birds that were autopsied, swab samples (mostly both cloacal and tracheal) were used for PCR analyses. The samples were analyzed for the detection of avian corona virus genome by using pancoronavirus qPCR targeting a 179-nt stretch of the RNA-dependent RNA polymerase (RdRp) gene. Positive samples were further analyzed with a second PCR targeting a 440 bp stretch of the CoV RdRp and the PCR product were analyzed by sequencing.